Att. #10

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lee, Jong Y.

(ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C., P.A.
(B) STREET: 60 South Sixth Street, Suite 3300
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/016,159
(B) FILING DATE: 30-JAN-1998

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/876,227
(B) FILING DATE: 16-JUN-1997

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/734,097
(B) FILING DATE: 21-OCT-1996

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/460,525
(B) FILING DATE: 02-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ellinger, Mark S.
(B) REGISTRATION NUMBER: 34,812
(C) REFERENCE/DOCKET NUMBER: 07004/002004

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 612/335-5070
(B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: BamHl linker ar 5' end followed by sequence for amino acids 25 through 29 of the full length human Epor protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC 23
Ala Pro Pro Pro
1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: EcoR1 linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human EpoR protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCGGG GTCCAGGTCG CT 22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
(B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:
(A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Smith, D.B.
Johnson, K.S.
(B) TITLE: Single-step purification of polypeptides expressed in Escherichia coli as fusions with glutathione-S-transferase
(D) VOLUME: 67
(F) PAGES: 31-40
(G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CTG GTT CCG CGT GGA  T CC                                              18
Leu Val Pro Arg Gly
  5
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Winkelmann , J. C., et al.
(C) JOURNAL: Blood
(D) VOLUME: 76
(E) ISSUE: 1
(F) PAGES: 24-30
(G) DATE: 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT      48
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
 1               5                  10                  15

CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC      96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
            20                  25                  30

CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA     144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
        35                  40                  45

GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG     192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
    50                  55                  60

GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC     240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65                  70                  75                  80

TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT     288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
                85                  90                  95
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CCC ACG GCT CGT GGT CGG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC      336
Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
            100                 105                 110

GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC      384
Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
        115                 120                 125

GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC      432
Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
    130                 135                 140

CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC      480
Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145                 150                 155                 160

CAC GTA GTG TTG CGC TGG CTC CCG CCG CCT GAG ACA CCC ATG ACG TCT      528
His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
                165                 170                 175

CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC CGG CCA GGG AGC      576
His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
            180                 185                 190

GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC      624
Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
        195                 200                 205

AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CGC GCG CGT ATG      672
Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
    210                 215                 220

GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG      720
Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225                 230                 235                 240

TCG CTG CTG GAG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC      768
Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
                245                 250                 255

CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC      816
Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
            260                 265                 270

TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC      864
Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
        275                 280                 285

CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC      912
Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
    290                 295                 300

CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC      960
Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
305                 310                 315                 320

ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG     1008
Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
                325                 330                 335

CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG     1056
Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
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                340                 345                 350

GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT     1104
Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
        355                 360                 365

CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC     1152
Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
    370                 375                 380

CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC     1200
Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
385                 390                 395                 400

TCA GAA GCA TCC TCC TGC TCA TCT GCT TTG GCC TCG AAG CCC AGC CCA     1248
Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
                405                 410                 415

GAG GGA GCC TCT GCT GCC AGC TTT GAG TAC ACT ATC CTG GAC CCC AGC     1296
Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
            420                 425                 430

TCC CAG CTC TTG CGT CCA TGG ACA CTG TGC CCT GAG CTG CCC CCT ACC     1344
Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
        435                 440                 445

CCA CCC CAC CTA AAG TAC CTG TAC CTT GTG GTA TCT GAC TCT GGC ATC     1392
Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
    450                 455                 460

TCA ACT GAC TAC AGC TCA GGG GAC TCC CAG GGA GCC CAA GGG GGC TTA     1440
Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
465                 470                 475                 480

TCC GAT GGG CCC TAC TCC AAC CCT TAT GAG AAC AGC CTT ATC CCA GCC     1488
Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
                485                 490                 495

GCT GAG CCT CTG CCC CCC AGC TAT GTG GCT TGC TCT TAG                 1527
Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
            500                 505
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
 1               5                  10                  15

Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
            20                  25                  30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
        35                  40                  45
```

```
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50                  55                  60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
65                  70                  75                  80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
                85                  90                  95

Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
            100                 105                 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
        115                 120                 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
    130                 135                 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
145                 150                 155                 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
                165                 170                 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
            180                 185                 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
        195                 200                 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
    210                 215                 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
225                 230                 235                 240

Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
                245                 250                 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
            260                 265                 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
        275                 280                 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
    290                 295                 300

Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
305                 310                 315                 320

Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
                325                 330                 335

Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
            340                 345                 350

Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
        355                 360                 365

Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
    370                 375                 380
```

Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
385 390 395 400

Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
405 410 415

Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
420 425 430

Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
435 440 445

Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
450 455 460

Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
465 470 475 480

Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
485 490 495

Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
500 505